

This listing of claims will replace all prior versions, and listings, of claims in the application.

**Listing of Claims:**

1. (Previously presented) A method for generating antibiotic resistant bacteria comprising the steps of:

introducing a dominant negative allele of a mismatch repair gene into said bacterium whereby said bacterium becomes hypermutable;  
contacting said bacterium with a plurality of antibiotics;  
selecting a bacterium that is resistant to said plurality of antibiotics; and  
culturing said bacterium;

thereby generating antibiotic resistant bacteria.

2. (Canceled)

3. (Currently amended) The method of claim 21 wherein said dominant negative allele of a mismatch repair gene is a *PMS2-134* gene.

4-13. (Canceled)

14. (Previously presented) The method of claim 1 wherein said plurality of antibiotics comprises a quinilone.

15. (Previously presented) The method of claim 1 wherein said plurality of antibiotics comprises an aminoglycoside.

16. (Previously presented) The method of claim 1 wherein said plurality of antibiotics comprises a magainin.

17. (Previously presented) The method of claim 1 wherein said plurality of antibiotics comprises a defensin.

18. (Previously presented) The method of claim 1 wherein said plurality of antibiotics comprises a tetracycline.

19. (Previously presented) The method of claim 1 wherein said plurality of antibiotics comprises a beta-lactam.

20. (Previously presented) The method of claim 1 wherein said plurality of antibiotics comprises a macrolide.

21. (Previously presented) The method of claim 1 wherein said plurality of antibiotics comprises a licosamide.

22. (Previously presented) The method of claim 1 wherein said plurality of antibiotics comprises a sulfonamide.

23. (Previously presented) The method of claim 1 wherein said plurality of antibiotics comprises a chloramphenicol.

24. (Previously presented) The method of claim 1 wherein said plurality of antibiotics comprises a nitrofurantoin.

25. (Previously presented) The method of claim 1 wherein said plurality of antibiotics comprises a isoniazid.

26. (Canceled)

27. (Original) The method of claim 1 further comprising making antibiotic resistant bacteria genetically stable.

28-37. (Canceled)

38. (Previously presented) An antibiotic resistant bacterium wherein said bacterium is resistant to a plurality of antibiotics, and wherein said bacterium comprises a dominant negative allele of a mismatch repair gene.

39-41. (Canceled)

42. (Previously presented) The antibiotic resistant bacteria of claim 38 wherein said dominant negative allele of a mismatch repair gene is *PMS2-134*.

43. (New) A method for generating antibiotic resistant bacteria comprising the steps of:

introducing a dominant negative allele of a mismatch repair gene into said bacterium whereby said bacterium becomes hypermutable;

contacting said bacterium with a plurality of antibiotics;

selecting a bacterium that is resistant to said plurality of antibiotics; and

culturing said bacterium;

thereby generating antibiotic resistant bacteria,

wherein said plurality of antibiotics comprises a quinilone, a magainin, a defensin, a tetracycline, a beta-lactam, a macrolide, a licosamide, a sulfonamide, a chloramphenicol, a nitrofurantoin, an isoniazid, or vancomycin.

44. (New) The method of claim 43 wherein said dominant negative allele of a mismatch repair gene is a *PMS2-134* gene.

45. (New) The method of claim 43 wherein said dominant negative allele of a mismatch repair gene is a *PMSR3* gene.

46. (New) The method of claim 43 further comprising making antibiotic resistant bacteria genetically stable.

47. (New) The method of claim 43 wherein said plurality of antibiotics further comprises an aminoglycoside.

48. (New) An antibiotic resistant bacterium wherein said bacterium is resistant to a plurality of antibiotics comprising a quinilone, a magainin, a defensin, a tetracycline, a beta-lactam, a macrolide, a licosamide, a sulfonamide, a chloramphenicol, a nitrofurantoin, an isoniazid, or vancomycin, and wherein said bacterium comprises a dominant negative allele of a mismatch repair gene.

49. (New) The antibiotic resistant bacteria of claim 48 wherein said dominant negative allele of a mismatch repair gene is *PMS2-134*.

50. (New) The antibiotic resistant bacteria of claim 48 wherein said dominant negative allele of a mismatch repair gene is *PMSR3*.